

SEQUENCE LISTING

<110> BASF Aktiengesellschaft

<120> The N-terminal β -barrel structure of lipid body
lipoxxygenase mediates its binding to liposomes and
lipid bodies [sic]

<130> 99_1235

<140>

<141>

<160> 4

<170> PatentIn Vers. 2.0

<210> 1

<211> 732

<212> DNA

<213> Cucumis sativus

<220>

<221> CDS

<222> (1)..(732)

<400> 1

atg ttt gga att ggg aag aac atc att gaa ggg gcc ttg aat aca act	48
Met Phe Gly Ile Gly Lys Asn Ile Ile Glu Gly Ala Leu Asn Thr Thr	
1 5 10 15	
gga gat ctt gca ggt tct gtt atc aat gct ggt ggt aac att tta gat	96
Gly Asp Leu Ala Gly Ser Val Ile Asn Ala Gly Gly Asn Ile Leu Asp	
20 25 30	
aga gtt tcc agt ctt gga gga aac aaa atc aaa ggg aaa gtg att ctt	144
Arg Val Ser Ser Leu Gly Gly Asn Lys Ile Lys Gly Lys Val Ile Leu	
35 40 45	
atg aga agc aat gtt ttg gat ttc act gaa ttt cat tcc aat ctt ctt	192
Met Arg Ser Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu	
50 55 60	
gat aac ttc act gag ctc ttg ggt ggt ggt gtt tct ttc caa ctc att	240
Asp Asn Phe Thr Glu Leu Leu Gly Gly Gly Val Ser Phe Gln Leu Ile	
65 70 75 80	
agt gcc act cat act tca aat gac tca aga ggg aaa gtt ggg aac aag	288
Ser Ala Thr His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys	
85 90 95	

gca tat ttg gag agg tgg cta act tca atc cca cca ctg ttt gct gga 336
 Ala Tyr Leu Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly
 100 105 110

gaa tca gtg ttc caa atc aac ttt caa tgg gat gaa aat ttt gga ttt 384
 Glu Ser Val Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe
 115 120 125

cca gga gct ttc ttc ata aaa aat gga cat aca agt gaa ttc ttt ctc 432
 Pro Gly Ala Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu
 130 135 140

aaa tct ctc act ctt gat gat gtt cct ggc tat ggc aga gtc cat ttt 480
 Lys Ser Leu Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe
 145 150 155 160

gat tgc aat tct tgg gtt tac cct tct gga aga tac aag aaa gat cgc 528
 Asp Cys Asn Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg
 165 170 175

att ttc ttt gcc aat cat gtt tat ctt cca agt caa aca cca aac cct 576
 Ile Phe Phe Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro
 180 185 190

ctt cgt aag tat aga gag gaa gaa ttg tgg aat ttg aga gga gat gga 624
 Leu Arg Lys Tyr Arg Glu Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly
 195 200 205

aca gga gaa aga aag gaa tgg gat aga att tat gac tat gat gtt tat 672
 Thr Gly Glu Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr
 210 215 220

aat gac att gct gac cct gat gtt ggt gat cat cgt cct att ctc ggt 720
 Asn Asp Ile Ala Asp Pro Asp Val Gly Asp His Arg Pro Ile Leu Gly
 225 230 235 240

ggg acg acc gaa 732
 Gly Thr Thr Glu

<210> 2

<211> 244

<212> PRT

<213> Cucumis sativus

<400> 2

Met Phe Gly Ile Gly Lys Asn Ile Ile Glu Gly Ala Leu Asn Thr Thr
 1 5 10 15

Gly Asp Leu Ala Gly Ser Val Ile Asn Ala Gly Gly Asn Ile Leu Asp
 20 25 30

Arg Val S r Ser Leu Gly Gly Asn Lys Ile Lys Gly Lys Val Ile Leu
 35 40 45

Met Arg Ser Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu
 50 55 60

Asp Asn Phe Thr Glu Leu Leu Gly Gly Gly Val Ser Phe Gln Leu Ile
 65 70 75 80

Ser Ala Thr His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys
 85 90 95

Ala Tyr Leu Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly
 100 105 110

Glu Ser Val Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe
 115 120 125

Pro Gly Ala Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu
 130 135 140

Lys Ser Leu Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe
 145 150 155 160

Asp Cys Asn Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg
 165 170 175

Ile Phe Phe Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro
 180 185 190

Leu Arg Lys Tyr Arg Glu Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly
 195 200 205

Thr Gly Glu Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr
 210 215 220

Asn Asp Ile Ala Asp Pro Asp Val Gly Asp His Arg Pro Ile Leu Gly
 225 230 235 240

Gly Thr Thr Glu

<210> 3

<211> 2964

<212> DNA

<213> Cucumis sativus

<220>

<221> CDS

<222> (48)..(2684)

<400> 3

```

gttccaaaca cacagtgagc aaaaaagaaa agtaaaaaag agtgaaa atg ttt gga      56
                                     Met Phe Gly
                                     1

att ggg aag aac atc att gaa ggg gcc ttg aat aca act gga gat ctt      104
Ile Gly Lys Asn Ile Ile Glu Gly Ala Leu Asn Thr Thr Gly Asp Leu
   5              10              15

gca ggt tct gtt atc aat gct ggt ggt aac att tta gat aga gtt tcc      152
Ala Gly Ser Val Ile Asn Ala Gly Gly Asn Ile Leu Asp Arg Val Ser
  20              25              30              35

agt ctt gga gga aac aaa atc aaa ggg aaa gtg att ctt atg aga agc      200
Ser Leu Gly Gly Asn Lys Ile Lys Gly Lys Val Ile Leu Met Arg Ser
              40              45              50

aat gtt ttg gat ttc act gaa ttt cat tcc aat ctt ctt gat aac ttc      248
Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu Asp Asn Phe
              55              60              65

act gag ctc ttg ggt ggt ggt gtt tct ttc caa ctc att agt gcc act      296
Thr Glu Leu Leu Gly Gly Gly Val Ser Phe Gln Leu Ile Ser Ala Thr
              70              75              80

cat act tca aat gac tca aga ggg aaa gtt ggg aac aag gca tat ttg      344
His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys Ala Tyr Leu
              85              90              95

gag agg tgg cta act tca atc cca cca ctg ttt gct gga gaa tca gtg      392
Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly Glu Ser Val
  100              105              110              115

ttc caa atc aac ttt caa tgg gat gaa aat ttt gga ttt cca gga gct      440
Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe Pro Gly Ala
              120              125              130

ttc ttc ata aaa aat gga cat aca agt gaa ttc ttt ctc aaa tct ctc      488
Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu Lys Ser Leu
              135              140              145

act ctt gat gat gtt cct ggc tat ggc aga gtc cat ttt gat tgc aat      536
Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe Asp Cys Asn
              150              155              160

tct tgg gtt tac cct tct gga aga tac aag aaa gat cgc att ttc ttt      584
Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg Ile Phe Phe
  165              170              175

```

gcc aat cat gtt tat ctt cca agt caa aca cca aac cct ctt cgt aag	632
Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro Leu Arg Lys	
180 185 190 195	
tat aga gag gaa gaa ttg tgg aat ttg aga gga gat gga aca gga gaa	680
Tyr Arg Glu Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly Thr Gly Glu	
200 205 210	
aga aag gaa tgg gat aga att tat gac tat gat gtt tat aat gac att	728
Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr Asn Asp Ile	
215 220 225	
gct gac cct gat gtt ggt gat cat cgt cct att ctc ggt ggg acg acc	776
Ala Asp Pro Asp Val Gly Asp His Arg Pro Ile Leu Gly Gly Thr Thr	
230 235 240	
gaa tat cct tac cct cgt agg gga aga aca gga cga cca cga tca aga	824
Glu Tyr Pro Tyr Pro Arg Arg Gly Arg Thr Gly Arg Pro Arg Ser Arg	
245 250 255	
aga gac cac aat tat gag agc aga ttg tca cca ata atg agc tta gac	872
Arg Asp His Asn Tyr Glu Ser Arg Leu Ser Pro Ile Met Ser Leu Asp	
260 265 270 275	
atc tat gta cca aaa gat gaa aac ttt ggg cat ttg aag atg tca gat	920
Ile Tyr Val Pro Lys Asp Glu Asn Phe Gly His Leu Lys Met Ser Asp	
280 285 290	
ttc ctt ggt tat aca tta aaa gca ctt tcg ata tca atc aaa cca gga	968
Phe Leu Gly Tyr Thr Leu Lys Ala Leu Ser Ile Ser Ile Lys Pro Gly	
295 300 305	
ctt caa tcc ata ttt gat gta act cca aat gaa ttt gac aat ttt aaa	1016
Leu Gln Ser Ile Phe Asp Val Thr Pro Asn Glu Phe Asp Asn Phe Lys	
310 315 320	
gaa gtt gat aat ctc ttt gag aga ggt ttt ccc att cca ttt aat gct	1064
Glu Val Asp Asn Leu Phe Glu Arg Gly Phe Pro Ile Pro Phe Asn Ala	
325 330 335	
ttt aag acc ctc act gag gac ctc act cca cct ttg ttc aaa gca ctc	1112
Phe Lys Thr Leu Thr Glu Asp Leu Thr Pro Pro Leu Phe Lys Ala Leu	
340 345 350 355	
gtg agg aat gat ggt gaa aaa ttc ctc aaa ttt cct act ccc gaa gtt	1160
Val Arg Asn Asp Gly Glu Lys Phe Leu Lys Phe Pro Thr Pro Glu Val	
360 365 370	
gtc aaa gat aat aaa ata gga tgg agc act gat gaa gaa ttt gca aga	1208
Val Lys Asp Asn Lys Ile Gly Trp Ser Thr Asp Glu Glu Phe Ala Arg	
375 380 385	

gaa atg tta gca gga ccc aat cct cta ttg att cgt cgt ctt gaa gct	1256
Glu Met Leu Ala Gly Pro Asn Pro Leu Leu Ile Arg Arg Leu Glu Ala	
390 395 400	
ttt cca cca aca agt aag ctt gac cca aat gtt tat ggg aat caa aac	1304
Phe Pro Pro Thr Ser Lys Leu Asp Pro Asn Val Tyr Gly Asn Gln Asn	
405 410 415	
agt acc atc act gaa gaa cac ata aag cat ggt tta gat ggt ctt acg	1352
Ser Thr Ile Thr Glu Glu His Ile Lys His Gly Leu Asp Gly Leu Thr	
420 425 430 435	
gtt gat gag gca atg aag caa aac agg ctc tac ata gtg gat ttc cat	1400
Val Asp Glu Ala Met Lys Gln Asn Arg Leu Tyr Ile Val Asp Phe His	
440 445 450	
gat gca tta atg ccc tat ctt aca agg atg aat gca aca tca aca aaa	1448
Asp Ala Leu Met Pro Tyr Leu Thr Arg Met Asn Ala Thr Ser Thr Lys	
455 460 465	
aca tat gcc aca aga aca ttg ctt ctt ttg aaa gat gat ggg act ttg	1496
Thr Tyr Ala Thr Arg Thr Leu Leu Leu Leu Lys Asp Asp Gly Thr Leu	
470 475 480	
aag cca ttg gtt att gag tta gcc ttg cca cat cct caa gga gat caa	1544
Lys Pro Leu Val Ile Glu Leu Ala Leu Pro His Pro Gln Gly Asp Gln	
485 490 495	
ctt ggt gcc att agc aaa cta tac ttt cca gct gaa aat gga gtt caa	1592
Leu Gly Ala Ile Ser Lys Leu Tyr Phe Pro Ala Glu Asn Gly Val Gln	
500 505 510 515	
aaa tcc att tgg caa ttg gct aaa gct tat gta act gtt aat gat gtt	1640
Lys Ser Ile Trp Gln Leu Ala Lys Ala Tyr Val Thr Val Asn Asp Val	
520 525 530	
ggc tac cat caa ctt att agt cat tgg ttg cat act cat gct gta ctt	1688
Gly Tyr His Gln Leu Ile Ser His Trp Leu His Thr His Ala Val Leu	
535 540 545	
gag cca ttt gtg att gca aca cat aga caa ttg agc gtg ctt cat cca	1736
Glu Pro Phe Val Ile Ala Thr His Arg Gln Leu Ser Val Leu His Pro	
550 555 560	
atc cat aag ttg ctt gtt cct cat tac aaa gac act atg ttt ata aat	1784
Ile His Lys L u L u Val Pro His Tyr Lys Asp Thr M t Phe Ile Asn	
565 570 575	
gca tct gca aga caa gtt ttg atc aat gcc aat ggt ctt atc gaa aca	1832
Ala Ser Ala Arg Gln Val Leu Ile Asn Ala Asn Gly Leu Ile Glu Thr	

580	585	590	595	
acc cat tat cca tca aaa tat tca atg gag ttg tca tct atc ttg tac				1880
Thr His Tyr Pro Ser Lys Tyr Ser Met Glu Leu Ser Ser Ile Leu Tyr				
	600	605	610	
aag gat tgg acc ttc cct gat caa gca tta cct aat aat ctc atg aag				1928
Lys Asp Trp Thr Phe Pro Asp Gln Ala Leu Pro Asn Asn Leu Met Lys				
	615	620	625	
aga gga cta gct gtg gag gac tca agt gcc ccc cat gga ctt aga ttg				1976
Arg Gly Leu Ala Val Glu Asp Ser Ser Ala Pro His Gly Leu Arg Leu				
	630	635	640	
cta ata aat gat tat cca ttt gct gtt gat ggt ctt gac att ttg tca				2024
Leu Ile Asn Asp Tyr Pro Phe Ala Val Asp Gly Leu Asp Ile Trp Ser				
	645	650	655	
gcc att aaa aca tgg gta cag gat tat tgc tgt ctc tac tac aaa gat				2072
Ala Ile Lys Thr Trp Val Gln Asp Tyr Cys Cys Leu Tyr Tyr Lys Asp				
	660	665	670	675
gac aat gca gta caa aat gac ttt gaa ctc caa tct tgg tgg aat gag				2120
Asp Asn Ala Val Gln Asn Asp Phe Glu Leu Gln Ser Trp Trp Asn Glu				
	680	685	690	
cta aga gag aaa ggc cac gct gac aag aaa cat gaa cca tgg tgg cca				2168
Leu Arg Glu Lys Gly His Ala Asp Lys Lys His Glu Pro Trp Trp Pro				
	695	700	705	
aaa atg caa act tta agt gaa tta atc gaa tcc tgc act aca att ata				2216
Lys Met Gln Thr Leu Ser Glu Leu Ile Glu Ser Cys Thr Thr Ile Ile				
	710	715	720	
tgg att gct tca gct ctt cat gcc gca gtt aac ttt gga caa tat ccc				2264
Trp Ile Ala Ser Ala Leu His Ala Ala Val Asn Phe Gly Gln Tyr Pro				
	725	730	735	
tac gga ggc tat att ctc aat cga cca act aca agt cgt agg ttc atg				2312
Tyr Gly Gly Tyr Ile Leu Asn Arg Pro Thr Thr Ser Arg Arg Phe Met				
	740	745	750	755
cct gaa gtt ggc acg gct gag tac aaa gaa ctg gaa tcg aat ccc gaa				2360
Pro Glu Val Gly Thr Ala Glu Tyr Lys Glu Leu Glu Ser Asn Pro Glu				
	760	765	770	
aaa gct ttc ttg aga aca ata tgt tca gaa tta caa gca ctt gtt agt				2408
Lys Ala Ph Leu Arg Thr Il Cys Ser Glu Leu Gln Ala Leu Val Ser				
	775	780	785	
att tca att att gaa atc ttg tca aag cat gct tct gat gaa gtt tat				2456

Ile S r Ile Ile Glu Ile Leu Ser Lys His Ala Ser Asp Glu Val Tyr
 790 795 800

ctt gga caa aga gct tca att gat tgg act tca gat aaa att gca ttg 2504
 Leu Gly Gln Arg Ala Ser Ile Asp Trp Thr Ser Asp Lys Ile Ala Leu
 805 810 815

gaa gca ttt gag aaa ttt ggg aaa aat tta ttt gaa gtt gag aat agg 2552
 Glu Ala Phe Glu Lys Phe Gly Lys Asn Leu Phe Glu Val Glu Asn Arg
 820 825 830 835

atc atg gaa agg aat aaa gag gtg aat ttg aag aat aga tct gga cct 2600
 Ile Met Glu Arg Asn Lys Glu Val Asn Leu Lys Asn Arg Ser Gly Pro
 840 845 850

gtt aat ttg cct tat act cta ctt gtt cca tca agt aac gaa gga ctc 2648
 Val Asn Leu Pro Tyr Thr Leu Leu Val Pro Ser Ser Asn Glu Gly Leu
 855 860 865

act gga aga gga att cct aat agt att tct atc taa gttgataaga 2694
 Thr Gly Arg Gly Ile Pro Asn Ser Ile Ser Ile
 870 875

aagaaaagtg gttcttttta tgggtgacgt gtgtaatttg aaggtcacaa attacatttt 2754
 aagttgcccc cattattatt atgaaggaaa taaatgacca tttttttagt ttaatttaaa 2814
 ttaggtagct atagccaact ttaggctctg ttggatttgg aactatctcc aacttatata 2874
 tgtactttgt actactattt gatgaataaa agttgtgtgt cttaagaata aaaaaaaaaa 2934
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2964

<210> 4
 <211> 878
 <212> PRT
 <213> Cucumis sativus

<400> 4
 Met Phe Gly Ile Gly Lys Asn Ile Ile Glu Gly Ala Leu Asn Thr Thr
 1 5 10 15
 Gly Asp Leu Ala Gly Ser Val Ile Asn Ala Gly Gly Asn Ile Leu Asp
 20 25 30
 Arg Val Ser Ser Leu Gly Gly Asn Lys Ile Lys Gly Lys Val Ile Leu
 35 40 45
 Met Arg Ser Asn Val Leu Asp Phe Thr Glu Phe His Ser Asn Leu Leu
 50 55 60

Asp Asn Ph Thr Glu Leu L u Gly Gly Gly Val Ser Phe Gln Leu Ile
 65 70 75 80

Ser Ala Thr His Thr Ser Asn Asp Ser Arg Gly Lys Val Gly Asn Lys
 85 90 95

Ala Tyr Leu Glu Arg Trp Leu Thr Ser Ile Pro Pro Leu Phe Ala Gly
 100 105 110

Glu Ser Val Phe Gln Ile Asn Phe Gln Trp Asp Glu Asn Phe Gly Phe
 115 120 125

Pro Gly Ala Phe Phe Ile Lys Asn Gly His Thr Ser Glu Phe Phe Leu
 130 135 140

Lys Ser Leu Thr Leu Asp Asp Val Pro Gly Tyr Gly Arg Val His Phe
 145 150 155 160

Asp Cys Asn Ser Trp Val Tyr Pro Ser Gly Arg Tyr Lys Lys Asp Arg
 165 170 175

Ile Phe Phe Ala Asn His Val Tyr Leu Pro Ser Gln Thr Pro Asn Pro
 180 185 190

Leu Arg Lys Tyr Arg Glu Glu Glu Leu Trp Asn Leu Arg Gly Asp Gly
 195 200 205

Thr Gly Glu Arg Lys Glu Trp Asp Arg Ile Tyr Asp Tyr Asp Val Tyr
 210 215 220

Asn Asp Ile Ala Asp Pro Asp Val Gly Asp His Arg Pro Ile Leu Gly
 225 230 235 240

Gly Thr Thr Glu Tyr Pro Tyr Pro Arg Arg Gly Arg Thr Gly Arg Pro
 245 250 255

Arg Ser Arg Arg Asp His Asn Tyr Glu Ser Arg Leu Ser Pro Ile Met
 260 265 270

Ser Leu Asp Ile Tyr Val Pro Lys Asp Glu Asn Phe Gly His Leu Lys
 275 280 285

Met Ser Asp Phe Leu Gly Tyr Thr Leu Lys Ala Leu Ser Ile Ser Ile
 290 295 300

Lys Pro Gly Leu Gln Ser Ile Phe Asp Val Thr Pro Asn Glu Phe Asp
 305 310 315 320

Asn Phe Lys Glu Val Asp Asn Leu Phe Glu Arg Gly Phe Pro Ile Pro
 325 330 335

Ph Asn Ala Phe Lys Thr L u Thr Glu Asp L u Thr Pro Pro Leu Phe
 340 345 350
 Lys Ala Leu Val Arg Asn Asp Gly Glu Lys Phe Leu Lys Phe Pro Thr
 355 360 365
 Pro Glu Val Val Lys Asp Asn Lys Ile Gly Trp Ser Thr Asp Glu Glu
 370 375 380
 Phe Ala Arg Glu Met Leu Ala Gly Pro Asn Pro Leu Leu Ile Arg Arg
 385 390 395 400
 Leu Glu Ala Phe Pro Pro Thr Ser Lys Leu Asp Pro Asn Val Tyr Gly
 405 410 415
 Asn Gln Asn Ser Thr Ile Thr Glu Glu His Ile Lys His Gly Leu Asp
 420 425 430
 Gly Leu Thr Val Asp Glu Ala Met Lys Gln Asn Arg Leu Tyr Ile Val
 435 440 445
 Asp Phe His Asp Ala Leu Met Pro Tyr Leu Thr Arg Met Asn Ala Thr
 450 455 460
 Ser Thr Lys Thr Tyr Ala Thr Arg Thr Leu Leu Leu Lys Asp Asp
 465 470 475 480
 Gly Thr Leu Lys Pro Leu Val Ile Glu Leu Ala Leu Pro His Pro Gln
 485 490 495
 Gly Asp Gln Leu Gly Ala Ile Ser Lys Leu Tyr Phe Pro Ala Glu Asn
 500 505 510
 Gly Val Gln Lys Ser Ile Trp Gln Leu Ala Lys Ala Tyr Val Thr Val
 515 520 525
 Asn Asp Val Gly Tyr His Gln Leu Ile Ser His Trp Leu His Thr His
 530 535 540
 Ala Val Leu Glu Pro Phe Val Ile Ala Thr His Arg Gln Leu Ser Val
 545 550 555 560
 Leu His Pro Ile His Lys Leu Leu Val Pro His Tyr Lys Asp Thr Met
 565 570 575
 Phe Il Asn Ala Ser Ala Arg Gln Val Leu Ile Asn Ala Asn Gly Leu
 580 585 590
 Ile Glu Thr Thr His Tyr Pro Ser Lys Tyr Ser Met Glu Leu Ser Ser
 595 600 605

Ile L u Tyr Lys Asp Trp Thr Ph Pro Asp Gln Ala Leu Pro Asn Asn
 610 615 620

Leu Met Lys Arg Gly Leu Ala Val Glu Asp Ser Ser Ala Pro His Gly
 625 630 635 640

Leu Arg Leu Leu Ile Asn Asp Tyr Pro Phe Ala Val Asp Gly Leu Asp
 645 650 655

Ile Trp Ser Ala Ile Lys Thr Trp Val Gln Asp Tyr Cys Cys Leu Tyr
 660 665 670

Tyr Lys Asp Asp Asn Ala Val Gln Asn Asp Phe Glu Leu Gln Ser Trp
 675 680 685

Trp Asn Glu Leu Arg Glu Lys Gly His Ala Asp Lys Lys His Glu Pro
 690 695 700

Trp Trp Pro Lys Met Gln Thr Leu Ser Glu Leu Ile Glu Ser Cys Thr
 705 710 715 720

Thr Ile Ile Trp Ile Ala Ser Ala Leu His Ala Ala Val Asn Phe Gly
 725 730 735

Gln Tyr Pro Tyr Gly Gly Tyr Ile Leu Asn Arg Pro Thr Thr Ser Arg
 740 745 750

Arg Phe Met Pro Glu Val Gly Thr Ala Glu Tyr Lys Glu Leu Glu Ser
 755 760 765

Asn Pro Glu Lys Ala Phe Leu Arg Thr Ile Cys Ser Glu Leu Gln Ala
 770 775 780

Leu Val Ser Ile Ser Ile Ile Glu Ile Leu Ser Lys His Ala Ser Asp
 785 790 795 800

Glu Val Tyr Leu Gly Gln Arg Ala Ser Ile Asp Trp Thr Ser Asp Lys
 805 810 815

Ile Ala Leu Glu Ala Phe Glu Lys Phe Gly Lys Asn Leu Phe Glu Val
 820 825 830

Glu Asn Arg Ile Met Glu Arg Asn Lys Glu Val Asn Leu Lys Asn Arg
 835 840 845

Ser Gly Pro Val Asn Leu Pro Tyr Thr Leu Leu Val Pro S r Ser Asn
 850 855 860

Glu Gly Leu Thr Gly Arg Gly Ile Pro Asn Ser Ile Ser Ile
 865 870 875